

AMENDMENTS TO THE SPECIFICATION:

Please cancel the specification, without prejudice and add the attached substitute specification in accordance with 37 C.F.R 1.125(b).

Please insert the sequence listing after the specification but before the listing of claims.

On page 1, line 5, after the Title, but before line 6, please insert the following new paragraph:

INCORPORATION OF SEQUENCE LISTING

Incorporated herein by reference in its entirety is the Sequence Listing for the application. The Sequence Listing is disclosed on a computer-readable ASCII text file titled, "sequence_listing.txt", created on September 18, 2008. The sequence_listing.txt file is 387 kb in size.

Please delete the paragraph on page 6, line 1 to line 19. Please replace it with the following:

Functional interaction between RKS and SBP proteins was shown by studies in transgenic tobacco plants in which SBP5 and RKS0 were both overexpressed under the control of an enhanced 35S promoter (data not shown). At the tip of double overexpressing plants, embryo structures appeared whereas in

the SBP5 overexpressing plants alone or the RKS0 overexpressing plants alone no phenotype was detectable at the root tips of transgenic tobacco plants. These results show that both RKS and SBP proteins are involved together in a signalling cascade, resulting in the reprogramming of developmental fate of a determined meristem. (ref. dissertation: <http://www.ab.uni-koeln.de/ediss/archiv/2001/11w1204.pdf>; Plant Journal 1997: 12, 2 367-377; Mol. Gen. Genet. 1996: 250, 7-16; Gene 1999, 237, 91-104, Genes and Development 1997: 11, 616-628), Proc. Natl. Acad. Sci. USA 1998: 95, 10306-10311; The Plant Journal 2000: 22, 523-529; Science 1997: 278, 1963-1965; Plant Physiol. Biochem. 2000: 38, 789-796; Cell 1996: 84, 61-71; Annu. Rev. Plant Physiol. Plant Mol. Biol. 1999: 50, 505-537

Please delete the paragraph on page 26, line 1 to line 5. Please replace it with the following:

That syntaxins and NDR/NHL genes share large homology becomes even more clear when performing a database search using the following site:
http://mips.gsf.de/proj/thal/db/search/search_frame.html
searching for homologous sequences with the sequence At1g32270

Please delete the paragraph on page 45, line 27 to line 29. Please replace it with the following:

Homology between aa sequences from arabidopsis proteins are compared with the rice databases using [\[\[:\]\]](http://mips.gsf.de/proj/thai/db/search/search_frame.html)
~~http://mips.gsf.de/proj/thai/db/search/search_frame.html~~ protein sequences based on Oryza sativa japonica contig sequences.

Please delete the paragraph on page 94, line 8 to line 32. Please replace it with the following:

The first domain of the predicted protein structure at the N-terminal end consists of a signal sequence, involved in targeting the protein towards the plasma membrane. Protein cleavage removes this sequence from the final mature protein product (Jain et al. 1994, J. Biol. Chemistry 269: 16306-16310). The second domain consists of different numbers of leucine zipper motifs, and is likely to be involved in protein protein dimerization. The next domain contains a conserved pair of cystein residues, involved in disulphate bridge formation. The next domain consists of 5 (or in the case of RKS3 only 4) leucine rich repeats (LRRs) shown in a gray colour, likely to be involved in ligand binding (Kobe and Deisenhofer 1994, TIBS 19: 415-420). This domain is again bordered by a domain containing a conserved pair of cystein residues involved in disulphate bridge formation often followed by a serine / proline rich region. The next domain displays all the characteristics of a single transmembrane domain (~~<http://genome.ebs.dtu.dk/services/TMHMM/>~~). At the

predicted cytoplasmic site of protein a domain is situated with unknown function, followed by a domain with serine/threonine kinase activity (Schmidt et al. 1997, Development 124: 2049-2062). The kinase domain is followed by a domain with unknown function whereas at the C-terminal end of the protein part of a leucine rich repeat is positioned, probably involved in protein-protein interactions.